

Amendments to the Specification

Please replace the paragraphs beginning at page 4, line 23, and ending at page 5, line 8, with the following amended paragraphs.

Figures 1-6 each depict an alignment of the amino acid sequence of a kinase of the invention (top line) with the conserved amino acid residues of the family of protein serine/threonine kinases (bottom line). Invariant residues are shown in UPPER CASE letters, nearly-invariant residues as lower case, conserved hydrophobic residues as (o), conserved polar residues as (*), and conserved small residues with near neutral polarity as (+).

Figure 1 presents the amino acid sequence alignment of the consensus protein serine/threonine kinase sequence with MDCK-1 (SEQ ID NO:8).

Figure 2 presents the amino acid sequence alignment of the consensus protein serine/threonine kinase sequence with MDCK-2 (SEQ ID NO:9).

Figure 3 presents the amino acid sequence alignment of the consensus protein serine/threonine kinase sequence with MDCK-3 (SEQ ID NO:10).

Figure 4 presents the amino acid sequence alignment of the consensus protein serine/threonine kinase sequence with MLSK-1 (SEQ ID NO:11).

Figure 5 presents the amino acid sequence alignment of the consensus protein serine/threonine kinase sequence with MLSK-2 (SEQ ID NO:12).

Figure 6 presents the amino acid sequence alignment of the consensus protein serine/threonine kinase sequence with LNRK-1 (SEQ ID NO:14).